CLAIMS

1.          A method of comparing spectral data or like data, which method comprises

defining as a group, a plurality of data points within a range of data points for a data item,

converting said group of data points to at least one kernel function, assembling the resultant

plurality of kernel functions covering all the data points for the data item into a cluster, and

projecting said cluster of kernel functions in high dimensional space using Cover's Theorem to

define a single searchable reference point for all the data points for said data item, and comparing

the said single searchable point for a sample item with the single searchable point for similarly

processed comparison items.

2.          A method as claimed in claim 1 characterised in that at least one of the groups of

data points is converted into a plurality of kernel functions.

3.          A method as claimed in claim 2 wherein the single searchable reference point is

defined by a vector function.

4.          A method as claimed in claim 1 wherein variables in data points within an item

define a radial basis function for the said single searchable point which constitute a measure of

the spread of said variables for that item about a mean.

5.          A method as claimed in claim 1 wherein uncertainty in the comparison of points is

resolved using transformations in possibility theory.

6.        A method as claimed in claim 1 wherein the data points are selected across a

range of data, in which the data is normalized by comparing all the data magnitudes as a

proportion of the highest, which is rated at 1.

7.        A method as claimed in claim 1 wherein the data is spectral data.

8.        An apparatus for screening of microorganisms characterised by spectroscopic

means for producing spectral data of the sample organism database means containing spectral

data for a range of microorganisms and comparison means for comparing the spectral data of the

sample with that of the database to permit classification/identification of the sample,

characterized in that the spectroscopic means comprises means for producing spectral data of the

sample organism by MALDI-TOF techniques and in that the database contains MALDI-TOF-MS

spectral data, and in that the comparison means is a method as claimed in claim 1.

9.        Apparatus as claimed in claim 8 wherein the spectral data in the database is

arranged in groups of data according to the genus of each microorganism with sub-divisions

corresponding to each strain of microorganism.

10.       Apparatus as claimed in claim 8 characterised in that the sample of unidentified

microorganism is prepared by a technique selected from the group consisting of (i) taking cells

from a culture and applying them to a sample plate comprising a matrix and (ii) by admixing the

cells with the matrix prior to subjecting to MALDI-TOF-MS analysis in order to retain the

cellular integrity of the sample.

11.          Apparatus as claimed in claim 6 characterised by means for bombarding a sample

matrix mixture with laser energy to create a gas phase ionic species which is then pulsed into a

flight conduit or tube for identification of both positive and/or negative ions.